CLAIMS

What is claimed is:

1. A method for estimating the precision of measurements taken from an array, comprising:

(a) identifying a set of low-level data measurements;

(b) estimating a standard deviation, σ_ε of an additive error component, ε;

(c) estimating a background parameter,α;

(d) identifying a set of replicated high-level data measurements;

(e) estimating a standard deviation, σ_η , from the standard deviation of the logarithm of the replicated high-level data set;

(f) measuring a signal, y, wherein said signal indicates an amount of a biological molecule; and

(g) estimating a variance of the measured signal as $\hat{\mathrm{Var}}(\hat{\mu}) = \hat{\sigma}_\varepsilon^2 + \hat{\mu}^2 e^{\hat{\sigma}_\eta^2}\left(e^{\hat{\sigma}_\eta^2} - 1\right)$, where $\hat{\mu}^2 = (y - \alpha)^2$.

2. The method of claim 1, wherein said identifying step (a) comprises the use of a thresholding algorithm to establish a cutoff, and the set of low-level data consists of those data with values less than the cutoff.

3. The method of claim 2, wherein the thresholding algorithm comprises the steps of:

(a) identifying A_N, an initial set of low-level data measurements consisting of q percent of the total number of data points having the lowest measurement values, $A_N = \{x_1, x_2, \ldots, x_{no}\}$;

(b) calculating a mean and a standard deviation of the initial set;

(c) calculating a cutoff point, u_N = mean plus c x the standard deviation, wherein $2 \leq c \leq 3$;

(d) defining a new set, $A_{N+1} = \{x_j < u_N\}$;

(e) calculating a mean and standard deviation of the new set; and

(f) repeating steps (c) and (d) using the mean and standard deviation of the new set until the algorithm converges.

4. The method of claim 2, wherein the thresholding algorithm comprises the steps of:

(a) identifying A_N, an initial set, of low-level data consisting of q percent of the total number of data points having the lowest measurement values, $A_N = \{x_1, x_2, \ldots, x_{no}\}$;

(b) calculating a median of the initial set, $m_o = \text{median}\ \{x_j\}_{j=1}^{n_o}$ and a median of the absolute deviations about the median, $MAD_0 = \text{median}\ \{|x_j - m_o|\}_{j=1}^{n_o}$;

(c) calculating a cutoff point, $u_0 = MAD_0 + c \text{ x } s_o$, wherein $s_o = MAD_0/0.675$ and $2 \leq c \leq 3$;

(d) defining a new set, $A_{N+1} = \{x_j < u_N\}$;

(e) calculating a median and a median of the absolute deviations about the median of the new set; and

(f) repeating steps (c) and (d) using the median and the median of the absolute deviations about the median of the new set until the algorithm converges.

5. The method of claim 2, wherein the mean of the low-level data measurements is used as the estimate of the background parameter, α.

6. The method of claim 1, wherein the standard deviation of the low-level data measurementsis used as the estimate of the parameter $\sigma_{\varepsilon.}$

7. The method of claim 1, wherein, a mean of negative control data is used as the estimate of the background parameter, α.

8. The method of claim 1, wherein the biological molecule is a nucleic acid.

9. The method of claim 8, wherein the nucleic acid is mRNA.

10. The method of claim 8, wherein the biological molecule is DNA.

11. The method of claim 10, wherein the DNA is cDNA.

12. The method of claim 10, wherein the DNA is genomic.

13. The method of claim 1, wherein the biological molecule is a protein.

14. The method of claim 1, wherein the biological molecule is a lipid.